

SEQUENCE LISTING

<110> FUKUCHI, Naoyuki
FUTAKI, Fumie
KITO, Morikazu
SATO, Seiichi
KAJIURA, Takayuki
ONO, Yukitsugu
TANAKA, Akiko
SHINOZAKI, Junko

<120> Substance with Antithrombic Activity and
Method for Detecting Glycocalicin

<130> OP818-PCT

<140> PCT/JP99/00089
<141> 1998-01-13

<150> JP 10-113962
<151> 1998-04-23

<160> 14

<170> PatentIn Ver. 2.0

<210> 1
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 1
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36

<210> 2
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<220>
<223> Description of Artificial Sequence:primer

<400> 2 atatctagat gtgcccgagg attgtggtt	29
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<220> <223> Description of Artificial Sequence:primer	
<400> 3 ataaaagcttc tcgagtcatt taccaggaga gtggga	36
<210> 4 <211> 684 <212> DNA <213> Mus musculus	
<220> <221> CDS <222> (1)..(684)	
<400> 4 gtg ccc agg gat tgt ggt tgt aag cct tgc ata tgt aca gtc cca gaa Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu 1 5 10 15 gta tca tct gtc ttc atc ttc ccc cca aag ccc aag gat gtg ctc acc Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr 20 25 30 att act ctg act cct aag gtc acg tgt gtt gtg gta gac atc agc aag Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys 35 40 45 gat gat ccc gag gtc cag ttc agc tgg ttt gta gat gat gtg gag gtg Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val 50 55 60 cac aca gct cag acg caa ccc cgg gag gag cag ttc aac agc act ttc His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe 65 70 75 80 cgc tca gtc agt gaa ctt ccc atc atg cac cag gac tgg ctc aat ggc Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly 85 90 95 aag gag ttc aaa tgc agg gta aac agt gca gct ttc cct gcc ccc atc	48 96 144 192 240 288 336

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile				
100	105	110		
gag aaa acc atc tcc aaa acc aaa ggc aga ccg aag gct cca cag gtg	384			
Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val				
115	120	125		
tac acc att cca cct ccc aag gag cag atg gcc aag gat aaa gtc agt	432			
Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser				
130	135	140		
ctg acc tgc atg ata aca gac ttc ttc cct gaa gac att act gtg gag	480			
Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu				
145	150	155	160	
tgg cag tgg aat ggg cag cca gcg gag aac tac aag aac act cag ccc	528			
Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro				
165	170	175		
atc atg gac aca gat ggc tct tac ttc gtc tac agc aag ctc aat gtg	576			
Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val				
180	185	190		
cag aag agc aac tgg gag gca gga aat act ttc acc tgc tct gtg tta	624			
Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu				
195	200	205		
cat gag ggc ctg cac aac cac cat act gag aag agc ctc tcc cac tct	672			
His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser				
210	215	220		
cct ggt aaa tga	684			
Pro Gly Lys				
225				

<210> 5

<211> 227

<212> PRT

<213> Mus musculus

<400> 5

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu			
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Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr			
20	25	30	

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys			
35	40	45	

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val			
50	55	60	

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe			
65	70	75	80

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 85 90 95
 Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 100 105 110
 Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 115 120 125
 Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 130 135 140
 Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 145 150 155 160
 Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 165 170 175
 Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
 180 185 190
 Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
 195 200 205
 His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
 210 215 220
 Pro Gly Lys
 225

<210> 6

<211> 1689

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of
genes of *Mus musculus* and *Homo sapiens*

<220>

<221> CDS

<222> (1)..(1689)

<220>

<221> sig_peptide

<222> (1)..(48)

<220>

<221> mat_peptide

<222> (49)..(1689)

<400> 6

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cac ccc atc tgt gag gtc tcc aaa gtg gcc agc cac cta gaa gtg aac His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn	1 5 10 15	96
tgt gac aag agg aat ctg aca gcg ctg cct cca gac ctg ccg aaa gac Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp	20 25 30	144
aca acc atc ctc cac ctg agt gag aac ctc ctg tac acc ttc tcc ctg Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu	35 40 45	192
gca acc ctg atg cct tac act cgc ctc act cag ctg aac cta gat agg Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg	50 55 60	240
tgc gag ctc acc aag ctc cag gtc gat ggg acg ctg cca gtg ctg ggg Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly	65 70 75 80	288
acc ctg gat cta tcc cac aat cag ctg caa agc ctg ccc ttg cta ggg Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly	85 90 95	336
cag aca ctg cct gct ctc acc gtc ctg gac gtc tcc ttc aac cgg ctg Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu	100 105 110	384
acc tcg ctg cct ctt ggt gcc ctg cgt ggt ctt ggc gaa ctc caa gag Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu	115 120 125	432
ctc tac ctg aaa ggc aat gag ctg aag acc ctg ccc cca ggg ctc ctg Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu	130 135 140	480
acg ccc aca ccc aag ctg gag aag ctc agt ctg gct aac aac aac ttg Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu	145 150 155 160	528
act gag ctc ccc gct ggg ctc ctg aat ggg ctg gag aat ctc gac acc Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr	165 170 175	576
ctt ctc ctc caa gag aac tcg ctg tat aca ata cca aag ggc ttt ttt Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe	180 185 190	624
ggg tcc cac ctc ctg cct ttt gct ttt ctc cac ggg aac ccc tgg tta Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu	195 200 205	672
tgc aac tgt gag atc ctc tat ttt cgt cgc tgg ctg cag gac aat gct	720	

Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala			
210	215	220	
gaa aat gtc tac gta tgg aag caa ggt gtg gac gtc aag gcc atg acc			768
Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr			
225	230	235	240
tct aac gtg gcc agt gtg cag tgt gac aat tca gac aag ttt ccc gtc			816
Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val			
245	250	255	
tac aaa tac cca gga aag ggg tgc ccc acc ctt ggt gat gaa ggt gac			864
Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp			
260	265	270	
aca gac cta tat gat tac tac cca gaa gag gac act gag ggc gat aag			912
Thr Asp Leu Tyr Asp Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys			
275	280	285	
gtg cgt gcc aca agg act gtg gtc aag ttc ccc acc aaa gcc cat aca			960
Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr			
290	295	300	
acc ccc tgg ggt cta ttc tac tca tgg tcc act gct tct cta gac gtg			1008
Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Val			
305	310	315	320
ccc agg gat tgt ggt tgt aag cct tgc ata tgt aca gtc cca gaa gta			1056
Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val			
325	330	335	
tca tct gtc ttc atc ttc ccc cca aag ccc aag gat gtg ctc acc att			1104
Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile			
340	345	350	
act ctg act cct aag gtc acg tgt gtt gtg gta gac atc agc aag gat			1152
Thr Leu Thr Pro Lys Val Thr Cys Val Val Asp Ile Ser Lys Asp			
355	360	365	
gat ccc gag gtc cag ttc agc tgg ttt gta gat gat gtg gag gtg cac			1200
Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His			
370	375	380	
aca gct cag acg caa ccc cgg gag gag cag ttc aac agc act ttc cgc			1248
Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg			
385	390	395	400
tca gtc agt gaa ctt ccc atc atg cac cag gac tgg ctc aat ggc aag			1296
Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys			
405	410	415	
gag ttc aaa tgc agg gta aac agt gca gct ttc cct gcc ccc atc gag			1344
Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu			
420	425	430	
aaa acc atc tcc aaa acc aaa ggc aga ccg aag gct cca cag gtg tac			1392
Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr			

435	440	445	
acc att cca cct ccc aag gag cag atg gcc aag gat aaa gtc agt ctg			1440
Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu			
450	455	460	
acc tgc atg ata aca gac ttc ttc cct gaa gac att act gtg gag tgg			1488
Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp			
465	470	475	480
cag tgg aat ggg cag cca gcg gag aac tac aag aac act cag ccc atc			1536
Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile			
485	490	495	
atg gac aca gat ggc tct tac ttc gtc tac agc aag ctc aat gtg cag			1584
Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln			
500	505	510	
aag agc aac tgg gag gca gga aat act ttc acc tgc tct gtg tta cat			1632
Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His			
515	520	525	
gag ggc ctg cac aac cac cat act gag aag agc ctc tcc cac tct cct			1680
Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro			
530	535	540	
ggt aaa tga			1689
Gly Lys			
545			

<210> 7

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of
genes of *Mus musculus* and *Homo sapiens*

<400> 7

Met Pro Leu Leu Leu Leu Leu Leu Pro Ser Pro Leu His Pro			
-16	-15	-10	-5

His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn			
1	5	10	15

Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp			
20	25	30	

Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu			
35	40	45	

Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg			
50	55	60	

Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly
 65 70 75 80
 Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly
 85 90 95
 Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu
 100 105 110
 Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu
 115 120 125
 Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu
 130 135 140
 Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu
 145 150 155 160
 Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr
 165 170 175
 Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe
 180 185 190
 Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu
 195 200 205
 Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala
 210 215 220
 Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr
 225 230 235 240
 Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val
 245 250 255
 Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp
 260 265 270
 Thr Asp Leu Tyr Asp Tyr Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys
 275 280 285
 Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr
 290 295 300
 Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Val
 305 310 315 320
 Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val
 325 330 335
 Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile
 340 345 350
 Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp
 355 360 365
 Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His
 370 375 380
 Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
 385 390 395 400
 Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys

405	410	415
Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu		
420	425	430
Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr		
435	440	445
Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu		
450	455	460
Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp		
465	470	475
Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile		
485	490	495
Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln		
500	505	510
Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His		
515	520	525
Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro		
530	535	540
Gly Lys		
545		

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 8
agcttaggatc cgagccccaga gggcccacaa 30

<210> 9
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 9
cccaagcttc tcgagacata cctttcattt acccggagtc cggga 44

<210> 10

<211> 729

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of genes of *Mus musculus* and *Homo sapiens*

<220>

<221> CDS

<222> (7)..(708)

<400> 10

ggatcc gag ccc aga ggg ccc aca atc aag ccc tgt cct cca tgc aaa 48

Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys

1 5 10

tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct 96
 Ser Pro Ala Pro Asn Ile Leu Gly Gly Pro Ser Val Phe Ile Phe Pro

Cys Pro Ala Tyr Asn Lys Lys Glu Glu Tyr Glu Val Val Val

15 20 25 30
cca aag atc aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca 144
Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr

35	40	45	
tgt gtg gtg gtg gat gtg agc gag gat gac cca gat gtc cag atc agc			192
Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser			
	55	60	

50	55	60	
tgg ttt gtg aac aac gtg gaa gta cac aca gct cag aca caa acc cat			240
Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His			
65	70	75	

aac aaa gac ctg cca gcg ccc atc gag aga acc atc tca aaa ccc aaa 384
 Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys

115	120	125	
ggg tca gta aga gct cca cag gta tat gtc ttg cct cca cca gaa gaa			432
Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu			
120	135	140	

130	135	140
gag atg act aag aaa cag gtc act ctg acc tgc atg gtc aca gac ttc		480
Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe		
145	150	155

atg cct gaa gac att tac gtg gag tgg acc aac aac ggg aaa aca gag 528

Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu
 160 165 170 576
 cta aac tac aag aac act gaa cca gtc ctg gac tct gat ggt tct tac
 Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr
 175 180 185 190 624
 ttc atg tac agc aag ctg aga gtg gaa aag aac tgg gtg gaa aga
 Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg
 195 200 205
 aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg cac aat cac cac
 Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His
 210 215 220
 acg act aag agc ttc tcc cg act ccg ggt aaa tgaaaggat gtctcgagaa 725
 Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
 225 230 729
 gctt

<210> 11

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of
genes of Mus musculus and Homo sapiens

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 Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
 1 5 10 15
 Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
 20 25 30
 Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
 35 40 45
 Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
 50 55 60
 Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
 65 70 75 80
 Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
 85 90 95
 Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
 100 105 110
 Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
 115 120 125
 Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Met

12/17

130 135 140
Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro
145 150 155 160
Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
165 170 175
Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
180 185 190
Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser
195 200 205
Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr
210 215 220
Lys Ser Phe Ser Arg Thr Pro Gly Lys
225 230

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 12

agcttatcttag acgagccca agggccccaca

30

<210> 13

<211> 1707

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of
genes of *Mus musculus* and *Homo sapiens*

<220>

<221> CDS

<222> (1)..(1707)

<220>

<221> sig_peptide

<222> (1)..(48)

<220>

<221> mat_peptide
<222> (49)..(1704)

<400>	13		48
atg cct ctc ctc ctc ttg ctg ctc ctg cca agc ccc tta cac ccc Met Pro Leu Leu Leu Leu Leu Leu Leu Pro Ser Pro Leu His Pro	-16	-15	
		-10	-5
cac ccc atc tgt gag gtc tcc aaa gtg gcc agc cac cta gaa gtg aac His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn	1	5	15
tgt gac aag agg aat ctg aca gcg ctg cct cca gac ctg ccg aaa gac Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp	20	25	30
aca acc atc ctc cac ctg agt gag aac ctc ctg tac acc ttc tcc ctg Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu	35	40	45
gca acc ctg atg cct tac act cgc ctc act cag ctg aac cta gat agg Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg	50	55	60
tgc gag ctc acc aag ctc cag gtc gat ggg acg ctg cca gtg ctg ggg Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly	65	70	75
acc ctg gat cta tcc cac aat cag ctg caa agc ctg ccc ttg cta ggg Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly	85	90	95
cag aca ctg cct gct ctc acc gtc ctg gac gtc tcc ttc aac cgg ctg Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu	100	105	110
acc tcg ctg cct ctt ggt gcc ctg cgt ggt ctt ggc gaa ctc caa gag Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu	115	120	125
ctc tac ctg aaa ggc aat gag ctg aag acc ctg ccc cca ggg ctc ctg Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu	130	135	140
acg ccc aca ccc aag ctg gag aag ctc agt ctg gct aac aac aac ttg Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu	145	150	155
act gag ctc ccc gct ggg ctc ctg aat ggg ctg gag aat ctc gac acc Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr	165	170	175
ctt ctc ctc caa gag aac tcg ctg tat aca ata cca aag ggc ttt ttt Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe	180	185	190

ggg tcc cac ctc ctg cct ttt gct ttt ctc cac ggg aac ccc tgg tta	672
Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu	
195 200 205	
tgc aac tgt gag atc ctc tat ttt cgt cgc tgg ctg cag gac aat gct	720
Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala	
210 215 220	
gaa aat gtc tac gta tgg aag caa ggt gtg gac gtc aag gcc atg acc	768
Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr	
225 230 235 240	
tct aac gtg gcc agt gtg cag tgt gac aat tca gac aag ttt ccc gtc	816
Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val	
245 250 255	
tac aaa tac cca gga aag ggg tgc ccc acc ctt ggt gat gaa ggt gac	864
Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp	
260 265 270	
aca gac cta tat gat tac tac cca gaa gag gac act gag ggc gat aag	912
Thr Asp Leu Tyr Asp Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys	
275 280 285	
gtg cgt gcc aca agg act gtg gtc aag ttc ccc acc aaa gcc cat aca	960
Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr	
290 295 300	
acc ccc tgg ggt cta ttc tac tca tgg tcc act gct tct cta gac gag	1008
Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Glu	
305 310 315 320	
ccc aga ggg ccc aca atc aag ccc tgt cct cca tgc aaa tgc cca gca	1056
Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala	
325 330 335	
cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct cca aag atc	1104
Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile	
340 345 350	
aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg	1152
Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val	
355 360 365	
gtg gat gtg agc gag gat gac cca gat gtc cag atc agc tgg ttt gtg	1200
Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val	
370 375 380	
aac aac gtg gaa gta cac aca gct cag aca caa acc cat aga gag gat	1248
Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp	
385 390 395 400	
tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag	1296
Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln	
405 410 415	
gac tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac	1344

Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp				
420	425	430		
ctg cca gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg tca gta				1392
Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val				
435	440	445		
aga gct cca cag gta tat gtc ttg cct cca cca gaa gaa gag atg act				1440
Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Glu Glu Glu Met Thr				
450	455	460		
aag aaa cag gtc act ctg acc tgc atg gtc aca gac ttc atg cct gaa				1488
Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu				
465	470	475	480	
gac att tac gtg gag tgg acc aac aac ggg aaa aca gag cta aac tac				1536
Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr				
485	490	495		
aag aac act gaa cca gtc ctg gac tct gat ggt tct tac ttc atg tac				1584
Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr				
500	505	510		
agc aag ctg aga gtg gaa aag aag aac tgg gtg gaa aga aat agc tac				1632
Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr				
515	520	525		
tcc tgt tca gtg gtc cac gag ggt ctg cac aat cac cac acg act aag				1680
Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys				
530	535	540		
agc ttc tcc cgg act ccg ggt aaa tga				1707
Ser Phe Ser Arg Thr Pro Gly Lys				
545	550			

<210> 14

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of
genes of Mus musculus and Homo sapiens

<400> 14

Met Pro Leu Leu Leu Leu Leu Leu Pro Ser Pro Leu His Pro
-16 -15 -10 -5His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn
1 5 10 15Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp
20 25 30

Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu
 35 40 45
 Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg
 50 55 60
 Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly
 65 70 75 80
 Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly
 85 90 95
 Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu
 100 105 110
 Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu
 115 120 125
 Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu
 130 135 140
 Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu
 145 150 155 160
 Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr
 165 170 175
 Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe
 180 185 190
 Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu
 195 200 205
 Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala
 210 215 220
 Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr
 225 230 235 240
 Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val
 245 250 255
 Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp
 260 265 270
 Thr Asp Leu Tyr Asp Tyr Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys
 275 280 285
 Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr
 290 295 300
 Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Glu
 305 310 315 320
 Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala
 325 330 335
 Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile
 340 345 350
 Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val
 355 360 365
 Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val

370	375	380
Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp		
385	390	395
Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln		
405	410	415
Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp		
420	425	430
Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val		
435	440	445
Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr		
450	455	460
Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu		
465	470	475
Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr		
485	490	495
Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr		
500	505	510
Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr		
515	520	525
Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys		
530	535	540
Ser Phe Ser Arg Thr Pro Gly Lys		
545	550	